Cont a5

sequence of the NDV fusion gene was identified. The sequence of this clone is given in SEQ ID NO: 1.--

On Page 19, line 24 to page 20, line 4 substitute the present pending paragraph with the following paragraph:

--Subgenomic Clone 407-32.2C3

a6 Cosmid 407-32.2C3 contains an approximately 40,000 base pair region of genomic HVT DNA (from the left terminus to position 39,750 GenBank Accession No. AF291866, see figure 2). This region includes NAHV *Bam*HI fragments F', L, P, N1, E, D, and 2,092 base pairs of fragment A'. Note: NAHV *Bam*HI fragment A', is called fragment B in HVT. This cosmid may be constructed as described above in the Procedure for Cloning NAHV Subgenomic DNA Fragments. It was isolated from the sheared DNA library by screening with the probes P1 (HVT *Bam*HI fragment F, position 116,948 to 125,961, Genbank Accession No. AF291866) and P2 (HVT *Bam*HI fragment B, 37,663 to 63,593, Genbank Accession No. AF291866). A bacterial strain containing this cosmid has been deposited pursuant to the Budapest Treaty on the International Deposit of Microorganisms for the Purposes of Patent Procedure with the Patent Culture Depository of the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia, 20110-2209 U.S.A. under ATCC Accession No. 75430.--

On Page 20, line 16 to page 20, line 28 substitute the present pending paragraph with the following paragraph:

a7 --Cosmid 407-32.5G6 contains a 39,404 base pair region of genomic HVT DNA (position 61,852 to 101,255, Genbank Accession No. AF291866). This region includes NAHV *Bam*HI fragments H, C, Q, K1, M, K2, plus 1,742 base pairs of fragment A', and

3,880 base pairs of fragment J. Note: NAHV *Bam*HI fragment A', is called fragment B in HVT. This cosmid was constructed as described above in the Procedure for Cloning NAHV Subgenomic DNA Fragments. It was isolated from the sheared DNA library by screening with the probes P2 (HVT *Bam*HI fragment B, 37,663 to 63,593, Genbank Accession No. AF291866) and P3 (HVT *Bam*HI fragment J, position 97,376 to 102,720, Genbank Accession No. AF291866). A bacterial strain containing this cosmid has been deposited on March 3, 1993 pursuant to the Budapest Treaty on the International Deposit of Microorganisms for the Purposes of Patent Procedure with the Patent Culture Depository of the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia, 20110-2209 U.S.A. under ATCC Accession No. 75427.--

On Page 20, line 30 to page 21, line 15 substitute the present pending paragraph with the following paragraph:

--Subgenomic Clone 407-32.1C1

Cosmid 407-32.1C1 contains a 37,444 base pair region of genomic HVT DNA (position 96,095 to 133,538, GenBank Accession No. AF291866, see figure 2). This region includes NAHV *Bam*HI fragments J, G, I, F, O, plus 1,281 base pairs of fragment K2, and 6,691 base pairs of fragment B'. Note: NAHV *Bam*HI fragment B', is called fragment A in HVT. This cosmid was constructed as described above in the Procedure for Cloning NAHV Subgenomic DNA Fragments. It was isolated from the sheared DNA library by screening with the probes P1 (HVT *Bam*HI fragment F, position 116,948 to 125,961, Genbank Accession No. AF291866) and P4 (4169 base pair *Bgl*II to *Stu*I sub-fragment (position 132,088 to 136,256, GenBank Accession No. AF291866) of HVT *Xho*I fragment #5 (position 128,950 to 136,510, GenBank Accession No. AF291866)). Note: an internal *Stu*I site occurs within the 4169 base pair sub-fragment (position

134,083, GenBank Accession No. AF291866). However this site is methylated and does not cleave in plasmid DNA prepared from standard cloning strains of bacteria. A bacterial strain containing this cosmid has been deposited on March 3, 1993 pursuant to the Budapest Treaty on the International Deposit of Microorganisms for the Purposes of Patent Procedure with the Patent Culture Depository of the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia, 20110-2209 U.S.A. under ATCC Accession No. 75428.--

On Page 22, line 8, to Page 22, line 16 substitute the present pending paragraph with the following paragraph:

--The cosmid 1002-75.4 contains a foreign gene encoding the fusion protein of the Newcastle disease virus inserted within the MDV US2 gene of the NAHV short region cosmid, 989-72.8#1. The NDV fusion gene (F) is under the control of the human cytomegalovirus immediate early (HCMV IE) promoter and utilizes the herpes simplex virus thymidine kinase (HSV tk) poly adenylation signal (pA). This cosmid was created using standard DNA cloning techniques. The sequence of the foreign DNA inserted into cosmid 989-72.8#1 is given in SEQ ID NO: 1. This sequence was inserted such that the NDV F and MDV US2 genes are transcribed in the same direction. The source of each region of the insert is indicated in the following table.--

On Page 22, line 20 to Page 22, line 21 substitute the present pending text with the following:

--[a] Starting position of the region in SEQ ID NO: 1

[b] Ending position of the region in SEQ ID NO: 1--

On Page 23, line 4, to Page 23 line 11 substitute the present pending paragraph with the following paragraph:

--The cosmid 1012-89.2 contains two foreign genes encoding the glycoprotein D and glycoprotein I of the infectious laryngotracheitis virus (ILTV) inserted in to the MDV US2 gene of the NAHV short region cosmid, 989-72.8#1. The ILTV genes are under the control of their endogenous promoters. This cosmid was created using standard DNA cloning techniques. The sequence of the foreign DNA inserted into cosmid 989-72.8#1 is given in SEQ ID NO: 3. This sequence was inserted such that the ILTV gD gene and ILTV gI gene are transcribed in the opposite direction of the MDV US2 genes. The source of each region of the insert is indicated in the following table. --

On Page 23, line 14 to Page 23, line 15 substitute the present pending text with the following:

--[a] Starting position of the region in SEQ ID NO: 3

[b] Ending position of the region in SEQ ID NO: 3--

On Page 23, line 20, to page 24, line 4 substitute the present pending paragraph with the following paragraph:

--The NAHV 295-01 recombinant virus was generated according to the Procedure for Generating Novel Avian Herpesvirus from Overlapping Subgenomic Fragments. The following combination of subgenomic clones and enzymes were used: 989-72.8#1 with I-*Sce*I, 407-32.2C3 with *Not*I, 172-07.BA2 with *Bam*HI, 407-32.5G6 with *Not*I, and 407-32.1C1 with *Not*I. (The location of subgenomic clones on the resulting NAHV genome is indicated in figure 2.) The NAHV was shown to have the

correct genomic structure using the Southern Blot Analysis of Novel Avian Herpesviruses. Stability of the NAHV 295-01 virus vaccine strain was demonstrated by serial passage 12 times in tissue culture followed by a second Southern blot analysis. This virus strain has been deposited pursuant to the Budapest Treaty on the International Deposit of Microorganisms for the Purposes of Patent Procedure with the Patent Culture Depository of the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia, 20110-2209 U.S.A. under ATCC Accession No. PTA-3451 on June 13, 2001.--

On page 25, line 16 to page 25, line 28 substitute the present pending paragraph with the following paragraph:

--The NAHV/NDV 295-93 recombinant virus was generated according to the Procedure for Generating Novel Avian Herpesvirus from Overlapping Subgenomic Fragments. The following combination of subgenomic clones and enzymes were used: 1002-75.4 with I-*Sce*I, 407-32.2C3 with *Not*I, 172-07.BA2 with *Bam*HI, 407-32.5G6 with *Not*I, and 407-32.1C1 with *Not*I. (The location of subgenomic clones on the resulting NAHV genome is indicated in figure 2.) The NAHV was shown to have the correct genomic structure using the Southern Blot Analysis of Novel Avian Herpesviruses. Stability of the NAHV/NDV 295-93 virus vaccine strain was demonstrated by serial passage 12 times in tissue culture followed by a second Southern blot analysis. This virus strain has been deposited pursuant to the Budapest Treaty on the International Deposit of Microorganisms for the Purposes of Patent Procedure with the Patent Culture Depository of the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia, 20110-2209 U.S.A. under ATCC Accession No. PTA-3453 on June 13, 2001.--

On Page 27, line 14 to page 27, line 26 substitute the present pending paragraph with the following paragraph:

--The NAHV/ILT 295-149 recombinant virus was generated according to the Procedure for Generating Novel Avian Herpesvirus from Overlapping Subgenomic Fragments. The following combination of subgenomic clones and enzymes were used: 1012-89.2 with I-*Sce*I, 407-32.2C3 with *Not*I, 172-07.BA2 with *Bam*HI, 407-32.5G6 with *Not*I, and 407-32.1C1 with *Not*I. (The location of subgenomic clones on the resulting NAHV genome is indicated in figure 2.) The NAHV was shown to have the correct genomic structure using the Southern Blot Analysis of Novel Avian Herpesviruses. Stability of the the NAHV/ILT 295-149 virus vaccine strain was demonstrated by serial passage 12 times in tissue culture followed by a second Southern blot analysis. This virus strain has been deposited pursuant to the Budapest Treaty on the International Deposit of Microorganisms for the Purposes of Patent Procedure with the Patent Culture Depository of the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia, 20110-2209 U.S.A. under ATCC Accession No. PTA-3452 on June 13, 2001.--